



1/6

SEQUENCE LISTING

<110> Bolk, Stacey
Daley, George Q.
McCarthy, Jeanette J.

<120> Association of Thrombospondin
Polymorphisms with Vascular Disease

<130> 2825.2025-001

<140> 10/007,781

<141> 2001-11-13

<150> 60/248,130

<151> 2000-11-13

<150> 60/300,158

<151> 2001-06-22

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5784

<212> DNA

<213> Homo sapiens

<400> 1

acggcatcca	gtacagaggg	gctggacttg	gacccctgca	gcagccctgc	acaggagaag	60
cggcatataa	agccgcgctg	cccgggagcc	gctcggccac	gtccaccgga	gcatcctgca	120
ctgcagggcc	ggtctctcgc	tccagcagag	cctgcgcctt	tctgactcgg	tccggaacac	180
tgaaccaggt	catcactgca	tctttttggc	aaaccaggag	ctcagctgca	ggaggcagga	240
tggtctggag	gctggctctg	ctggctctgt	gggtgtggcc	cagcacgcaa	gctggtcacc	300
aggacaaaga	cacgaccttc	gaccttttca	gtatcagcaa	catcaaccgc	aagaccattg	360
gcgccaagca	gttccgcggg	cccgaacccg	gcgtgccggc	ttaccgcttc	gtgcgctttg	420
actacatccc	accggtgaac	gcagatgacc	tcagcaagat	caccaagatc	atgcggcaga	480
aggagggttt	cttcctcacg	gcccagctca	agcaggacgg	caagtccagg	ggcacgctgt	540
tggtcttgga	gggccccggg	ctctcccaga	ggcagttcga	gatcgtctcc	aacggccccg	600
cggacacgct	ggatctcacc	tactggattg	acggcaccgc	gcattgtggtc	tccctggagg	660
acgtcggcct	ggctgactcg	cagtggaaaga	acgtcacccg	gcaggtggct	ggcgagacct	720
acagcttgca	cgtgggctgc	gacctcatag	gaccagttgc	tctggacgag	cccttctacg	780
agcacctgca	ggcggaagag	agccggatgt	acgtggccaa	aggctctgcc	agagagagtc	840
acttcagggg	tttgcttcag	aacgtccacc	tagtgtttga	aaactctgtg	gaagatattc	900
taagcaagaa	gggttgccag	caaggccagg	gagctgagat	caacgccatc	agtgagaaca	960
cagagacgct	gcgcctgggt	ccgcatgtca	ccaccgagta	cgtggggccc	agctcggaga	1020
ggaggcccga	ggtgtgcgaa	cgctcgtgcg	aggagctggg	aaacatggtc	caggagctct	1080
cggggctcca	cgtcctcgtg	aaccagctca	gcgagaacct	caagagagtg	tcgaatgata	1140
accagtttct	ctgggagctc	attggtggcc	ctcctaagac	aaggaacatg	tcagcttgct	1200
ggcaggatgg	ccggttcttt	gcggaagatg	aaacgtgggt	ggtggacagc	tgcaccacgt	1260
gtacctgcaa	gaaatttaaa	accatttgcc	accaaatac	ctgcccgcct	gcaacctgcg	1320
ccagtcctac	ctttgtggaa	ggcgaatgct	gcccttcctg	cctccactcg	gtggacgggtg	1380
aggagggtctg	gtctccgtgg	gcagagtggg	ccagtgctc	cgtgacgtgt	ggctctggga	1440
cccagcagag	aggccgggtcc	tgtgacgtca	ccagcaacac	ctgcttgggg	ccctcgatcc	1500
agacacgggg	ttgcagctcg	agcaagtgtg	acacccgcat	ccggcaggac	ggcggctgga	1560
gccactgggtc	accttgggtct	tcatgtctctg	tgacctgtgg	agttggcaat	atcacacgca	1620

tccgtctctg	caactcccca	gtgccccaga	tgggggggcaa	gaattgcaaa	gggagtgggc	1680
gggagaccaa	agcctgccag	ggcgccccat	gcccacatcga	tggccgctgg	agcccctggg	1740
ccccgtggtc	ggcctgcact	gtcacctgtg	ccgggtgggat	ccggggagcgc	acccgggtct	1800
gcaacagccc	tgagcctcag	tacggagggg	aggcctgcgt	gggggatgtg	caggagcgtc	1860
agatgtgcaa	caagaggagc	tgccccgtgg	atggctgttt	atccaacccc	tgcttcccgg	1920
gagcccagtg	cagcagcttc	cccgatgggt	cctgggtcatg	cggcttctgc	cctgtgggct	1980
tcttgggcaa	tggcaccac	tgtgaggacc	tggacgagtg	tgccctggtc	cccgcacatct	2040
gcttctccac	cagcaagggtg	cctcgctgtg	tcaacactca	gcctggcttc	cactgcctgc	2100
cctgccccgc	ccgatacaga	gggaaccagc	ccgtcgggggt	cggcctggaa	gcagccaaga	2160
cggaaaagca	agtgtgtgag	cccgaiaacc	catgcaagga	caagacacac	aactgccaca	2220
agcacgcgga	gtgcatctac	ctgggtcact	tcagcgaccc	catgtacaag	tgcgagtggc	2280
agacaggcta	cgcgggagac	gggtcatct	gcggggagga	ctcggaacctg	gacggctggc	2340
ccaacctcaa	tctggtctgc	gccaccaacg	ccacctacca	ctgcatcaag	gataactgcc	2400
cccatctgcc	aaattctggg	caggaagact	ttgacaagga	cgggattggc	gatgcctgtg	2460
atgatgaca	tgacaatgac	ggtgtgaccg	atgagaagga	caactgccag	ctcctcttca	2520
atccccgcca	ggctgacctat	gacaaggatg	aggttgggga	ccgctgtgac	aactgcccct	2580
acgtgcacaa	ccctgcccag	atcgacacag	acaacaatgg	agaggggtgac	gcctgtcccg	2640
tggacattga	tggggacgat	gtcttcaatg	aacgagacaa	ttgtccctac	gtctacaaca	2700
ctgaccagag	ggacacggat	ggtgacgggtg	tgggggatca	ctgtgacaac	tgccccctgg	2760
tgcacaaccc	tgaccagacc	gacgtggaca	atgaccttgt	tggggaccag	tgtgacaaca	2820
acgaggacat	agatgacgac	ggccaccaga	acaaccagga	caactgcccc	tacatctcca	2880
acgccaacca	ggctgacctat	gacagagacg	gccagggcga	cgctgtgac	cctgatgatg	2940
acaacgatgg	cgtccccgat	gacagggaca	actgcccgt	tgtgttcaac	ccagaccagg	3000
aggacttgga	cggatgatga	cgggggtgata	tttgtaaaga	tgattttgac	aatgacaaca	3060
tcccagatat	tgatgatgtg	tgtcctgaaa	acaatgccat	cagttagaca	gacttcagga	3120
acttccagat	ggtccccctg	gatcccaaaag	ggaccaccca	aattgatccc	aactgggtca	3180
ttcgccatca	aggcaaggag	ctggttcaga	cagccaactc	ggacccccggc	atcgctgtag	3240
gttttgacga	gtttgggtct	gtggacttca	gtggcacatt	ctacgtaaac	actgaccggg	3300
acgacgacta	tgtgtgcttc	gtctttgggt	accagtcaag	cagccgcttc	tatgtgggtga	3360
tgtggaagca	ggtgacgcag	acctactggg	aggaccagcc	cacgcggggc	tatggctact	3420
ccggcggtgc	cctcaagggtg	gtgaactcca	ccacggggac	gggcgagcac	ctgaggaacg	3480
cgctgtggga	cacggggaaac	acgcccggggc	aggtgcgaac	cttatggcac	gacccagga	3540
acattggctg	gaaggactac	acggcctata	ggtggcacct	gactcacagg	ccaagaccg	3600
gctacatcag	agtcttagtg	catgaaggaa	aacaggtcat	ggcagactca	ggacctatct	3660
atgaccaaac	ctacgctggc	gggcggctgg	gtctatattgt	cttctctcaa	gaaatgggtct	3720
atcttctcaga	cctcaagtag	gaatgcagag	atattttaaac	aagattttgct	gcatttccgg	3780
caatgccttg	tgcattgccat	ggtccctaga	cacctcagtt	cattgtgggtc	cttgcgggtt	3840
ctctctctag	cagcacctcc	tgtcccttga	ccttaactct	gatggttctt	cacctcctgc	3900
cagcaacccc	aaacccaagt	gccttcagag	gataaatac	aatggaactc	agagatgaac	3960
atctaaccga	ctagaggaaa	ccagtttggg	gatataatgag	actttatgtg	gagtgaatac	4020
tgggcatgcc	attacattgc	tttttcttgt	ttgtttaaaa	agaatgacgt	ttacataata	4080
aatgtaatta	cttattgtat	ttatgtgtat	atggagttga	aggaataact	gtgcataagc	4140
cattatgata	aattaagcat	gaaaaatatt	gctgaactac	ttttgggtgct	taaagtgtgc	4200
actattcttg	aattagagtt	gctctacaat	gacacacaaa	tcccgcataaa	taaattataa	4260
acaagggtca	attcaaattt	gaagtaattg	tttagtaagg	agagattaga	agacaacagg	4320
catagcaaat	gacataagct	accgattaac	taatcggaac	atgtaaaaaca	gttacaataa	4380
taaacgaact	ctcctcttgt	cctacaatga	aagccctcat	gtgcagtaga	gatgcagttt	4440
catcaaagaa	caaacatcct	tgcaaatggg	tgtgacgcgg	ttccagatgt	ggatttggca	4500
aaacctcatt	taagtaaaag	gttagcagag	caaagtgcgg	tgctttagct	gctgcttgtg	4560
ccgttggtgg	gtcggggagg	ctcctgcctg	agcttccttc	cccagctttg	ctgcctgaga	4620
ggaaccagag	cagacgcaca	ggccggaaaa	ggcgcatcta	acgcgtatct	aggctttggg	4680
aactgcggac	aagttgcttt	tacctgattt	ggtgatacat	ttcattaaag	ttccagttat	4740
aaataatttg	ttaatatatta	ttaagtgact	atagaatgca	actccattta	ccagtaactt	4800
attttaaata	tgcctagtaa	cacatatgta	gtataatttc	tagaaacaaa	catctaataa	4860
gtatataaat	ctgtgaaaaat	atgaggcttg	ataatattag	gttgctacga	tgaagcatgc	4920
tagaagctgt	aacagaatac	atagagaata	atgaggagtt	tatgatggaa	ccttaataata	4980
taatgttgcc	agcgattttt	gttcaatat	tgttactgtt	atctatctgc	tgtatatgga	5040
attcttttaa	ttcaaacgct	gaaaacgaat	cagcattttag	tcttgccagg	cacacccaat	5100
aatcagtcac	gtgtaatatg	cacaagtttg	tttttgtttt	tgtttttttt	ggttggttggt	5160

```

ttttttgctt taagttgcat gatctttctg caggaaatag tcactcatcc cactccacat 5220
aaggggttta gtaagagaag tctgtctgtc tgatgatgga tagggggcaa atctttttcc 5280
cctttctggt aatagtcacg acatttctat gccaaacagg aacgatccat aacttttagtc 5340
ttaatgtaca cattgcattt tgataaaaatt aattttgttg ttccctttga ggttgatcgt 5400
tgtgttggtt tgctgcactt tttacttttt tgcgtgtgga gctgtattcc cgagacaacg 5460
aagcgttggg atacttcatt aaatgtagcg actgtcaaca gcgtgcaggt tttctgtttc 5520
tgtgttggtg ggtcaaccgt acaatgggtg gggaatgacg atgatgtgaa tatttagaat 5580
gtaccatatt ttttgtaaatt tatttatgtt tttctaaaca aatttatcgt ataggttgat 5640
gaaacgtcat gtgttttggc aaagactgta aatatttatt tatgtgttca catggtcaaa 5700
atctcaccac tgaaaccctg cacttagcta gaacctcatt tttaaagatt aacaacagga 5760
aataaattgt aaaaaaggtt ttct

```

<210> 2
 <211> 1172
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	Val	Trp	Arg	Leu	Val	Leu	Leu	Ala	Leu	Trp	Val	Trp	Pro	Ser	Thr
1				5					10					15	
Gln	Ala	Gly	His	Gln	Asp	Lys	Asp	Thr	Thr	Phe	Asp	Leu	Phe	Ser	Ile
			20					25					30		
Ser	Asn	Ile	Asn	Arg	Lys	Thr	Ile	Gly	Ala	Lys	Gln	Phe	Arg	Gly	Pro
		35					40					45			
Asp	Pro	Gly	Val	Pro	Ala	Tyr	Arg	Phe	Val	Arg	Phe	Asp	Tyr	Ile	Pro
	50					55					60				
Pro	Val	Asn	Ala	Asp	Asp	Leu	Ser	Lys	Ile	Thr	Lys	Ile	Met	Arg	Gln
65					70					75				80	
Lys	Glu	Gly	Phe	Phe	Leu	Thr	Ala	Gln	Leu	Lys	Gln	Asp	Gly	Lys	Ser
			85						90					95	
Arg	Gly	Thr	Leu	Leu	Ala	Leu	Glu	Gly	Pro	Gly	Leu	Ser	Gln	Arg	Gln
		100						105					110		
Phe	Glu	Ile	Val	Ser	Asn	Gly	Pro	Ala	Asp	Thr	Leu	Asp	Leu	Thr	Tyr
		115					120					125			
Trp	Ile	Asp	Gly	Thr	Arg	His	Val	Val	Ser	Leu	Glu	Asp	Val	Gly	Leu
		130				135					140				
Ala	Asp	Ser	Gln	Trp	Lys	Asn	Val	Thr	Val	Gln	Val	Ala	Gly	Glu	Thr
145					150					155				160	
Tyr	Ser	Leu	His	Val	Gly	Cys	Asp	Leu	Ile	Gly	Pro	Val	Ala	Leu	Asp
			165						170					175	
Glu	Pro	Phe	Tyr	Glu	His	Leu	Gln	Ala	Glu	Lys	Ser	Arg	Met	Tyr	Val
		180						185					190		
Ala	Lys	Gly	Ser	Ala	Arg	Glu	Ser	His	Phe	Arg	Gly	Leu	Leu	Gln	Asn
		195					200					205			
Val	His	Leu	Val	Phe	Glu	Asn	Ser	Val	Glu	Asp	Ile	Leu	Ser	Lys	Lys
	210					215					220				
Gly	Cys	Gln	Gln	Gly	Gln	Gly	Ala	Glu	Ile	Asn	Ala	Ile	Ser	Glu	Asn
225					230					235				240	
Thr	Glu	Thr	Leu	Arg	Leu	Gly	Pro	His	Val	Thr	Thr	Glu	Tyr	Val	Gly
			245						250					255	
Pro	Ser	Ser	Glu	Arg	Arg	Pro	Glu	Val	Cys	Glu	Arg	Ser	Cys	Glu	Glu
		260						265					270		
Leu	Gly	Asn	Met	Val	Gln	Glu	Leu	Ser	Gly	Leu	His	Val	Leu	Val	Asn
		275					280					285			
Gln	Leu	Ser	Glu	Asn	Leu	Lys	Arg	Val	Ser	Asn	Asp	Asn	Gln	Phe	Leu
	290					295					300				
Trp	Glu	Leu	Ile	Gly	Gly	Pro	Pro	Lys	Thr	Arg	Asn	Met	Ser	Ala	Cys

305		310		315		320									
Trp	Gln	Asp	Gly	Arg	Phe	Phe	Ala	Glu	Asn	Glu	Thr	Trp	Val	Val	Asp
		325							330					335	
Ser	Cys	Thr	Thr	Cys	Thr	Cys	Lys	Lys	Phe	Lys	Thr	Ile	Cys	His	Gln
		340							345					350	
Ile	Thr	Cys	Pro	Pro	Ala	Thr	Cys	Ala	Ser	Pro	Ser	Phe	Val	Glu	Gly
		355						360					365		
Glu	Cys	Cys	Pro	Ser	Cys	Leu	His	Ser	Val	Asp	Gly	Glu	Glu	Gly	Trp
		370					375					380			
Ser	Pro	Trp	Ala	Glu	Trp	Thr	Gln	Cys	Ser	Val	Thr	Cys	Gly	Ser	Gly
385					390					395					400
Thr	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp	Val	Thr	Ser	Asn	Thr	Cys	Leu
			405						410					415	
Gly	Pro	Ser	Ile	Gln	Thr	Arg	Ala	Cys	Ser	Leu	Ser	Lys	Cys	Asp	Thr
			420					425						430	
Arg	Ile	Arg	Gln	Asp	Gly	Gly	Trp	Ser	His	Trp	Ser	Pro	Trp	Ser	Ser
		435					440					445			
Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn	Ile	Thr	Arg	Ile	Arg	Leu	Cys
		450				455					460				
Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly	Lys	Asn	Cys	Lys	Gly	Ser	Gly
465					470					475					480
Arg	Glu	Thr	Lys	Ala	Cys	Gln	Gly	Ala	Pro	Cys	Pro	Ile	Asp	Gly	Arg
			485						490					495	
Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	Cys	Thr	Val	Thr	Cys	Ala	Gly
		500						505					510		
Gly	Ile	Arg	Glu	Arg	Thr	Arg	Val	Cys	Asn	Ser	Pro	Glu	Pro	Gln	Tyr
		515					520					525			
Gly	Gly	Lys	Ala	Cys	Val	Gly	Asp	Val	Gln	Glu	Arg	Gln	Met	Cys	Asn
		530				535					540				
Lys	Arg	Ser	Cys	Pro	Val	Asp	Gly	Cys	Leu	Ser	Asn	Pro	Cys	Phe	Pro
545				550						555					560
Gly	Ala	Gln	Cys	Ser	Ser	Phe	Pro	Asp	Gly	Ser	Trp	Ser	Cys	Gly	Phe
			565						570					575	
Cys	Pro	Val	Gly	Phe	Leu	Gly	Asn	Gly	Thr	His	Cys	Glu	Asp	Leu	Asp
		580					585						590		
Glu	Cys	Ala	Leu	Val	Pro	Asp	Ile	Cys	Phe	Ser	Thr	Ser	Lys	Val	Pro
		595				600						605			
Arg	Cys	Val	Asn	Thr	Gln	Pro	Gly	Phe	His	Cys	Leu	Pro	Cys	Pro	Pro
		610			615						620				
Arg	Tyr	Arg	Gly	Asn	Gln	Pro	Val	Gly	Val	Gly	Leu	Glu	Ala	Ala	Lys
625				630						635					640
Thr	Glu	Lys	Gln	Val	Cys	Glu	Pro	Glu	Asn	Pro	Cys	Lys	Asp	Lys	Thr
			645						650					655	
His	Asn	Cys	His	Lys	His	Ala	Glu	Cys	Ile	Tyr	Leu	Gly	His	Phe	Ser
		660						665					670		
Asp	Pro	Met	Tyr	Lys	Cys	Glu	Cys	Gln	Thr	Gly	Tyr	Ala	Gly	Asp	Gly
		675					680					685			
Leu	Ile	Cys	Gly	Glu	Asp	Ser	Asp	Leu	Asp	Gly	Trp	Pro	Asn	Leu	Asn
		690				695					700				
Leu	Val	Cys	Ala	Thr	Asn	Ala	Thr	Tyr	His	Cys	Ile	Lys	Asp	Asn	Cys
705				710						715					720
Pro	His	Leu	Pro	Asn	Ser	Gly	Gln	Glu	Asp	Phe	Asp	Lys	Asp	Gly	Ile
			725						730					735	
Gly	Asp	Ala	Cys	Asp	Asp	Asp	Asp	Asp	Asn	Asp	Gly	Val	Thr	Asp	Glu
		740					745					750			
Lys	Asp	Asn	Cys	Gln	Leu	Leu	Phe	Asn	Pro	Arg	Gln	Ala	Asp	Tyr	Asp
		755					760					765			
Lys	Asp	Glu	Val	Gly	Asp	Arg	Cys	Asp	Asn	Cys	Pro	Tyr	Val	His	Asn
		770				775					780				

Pro Ala Gln Ile Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ser
 785 790 795 800
 Val Asp Ile Asp Gly Asp Asp Val Phe Asn Glu Arg Asp Asn Cys Pro
 805 810 815
 Tyr Val Tyr Asn Thr Asp Gln Arg Asp Thr Asp Gly Asp Gly Val Gly
 820 825 830
 Asp His Cys Asp Asn Cys Pro Leu Val His Asn Pro Asp Gln Thr Asp
 835 840 845
 Val Asp Asn Asp Leu Val Gly Asp Gln Cys Asp Asn Asn Glu Asp Ile
 850 855 860
 Asp Asp Asp Gly His Gln Asn Asn Gln Asp Asn Cys Pro Tyr Ile Ser
 865 870 875 880
 Asn Ala Asn Gln Ala Asp His Asp Arg Asp Gly Gln Gly Asp Ala Cys
 885 890 895
 Asp Pro Asp Asp Asp Asn Asp Gly Val Pro Asp Asp Arg Asp Asn Cys
 900 905 910
 Arg Leu Val Phe Asn Pro Asp Gln Glu Asp Leu Asp Gly Asp Gly Arg
 915 920 925
 Gly Asp Ile Cys Lys Asp Asp Phe Asp Asn Asp Asn Ile Pro Asp Ile
 930 935 940
 Asp Asp Val Cys Pro Glu Asn Asn Ala Ile Ser Glu Thr Asp Phe Arg
 945 950 955 960
 Asn Phe Gln Met Val Pro Leu Asp Pro Lys Gly Thr Thr Gln Ile Asp
 965 970 975
 Pro Asn Trp Val Ile Arg His Gln Gly Lys Glu Leu Val Gln Thr Ala
 980 985 990
 Asn Ser Asp Pro Gly Ile Ala Val Gly Phe Asp Glu Phe Gly Ser Val
 995 1000 1005
 Asp Phe Ser Gly Thr Phe Tyr Val Asn Thr Asp Arg Asp Asp Asp Tyr
 1010 1015 1020
 Ala Gly Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val
 1025 1030 1035 1040
 Met Trp Lys Gln Val Thr Gln Thr Tyr Trp Glu Asp Gln Pro Thr Arg
 1045 1050 1055
 Ala Tyr Gly Tyr Ser Gly Val Ser Leu Lys Val Val Asn Ser Thr Thr
 1060 1065 1070
 Gly Thr Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr
 1075 1080 1085
 Pro Gly Gln Val Arg Thr Leu Trp His Asp Pro Arg Asn Ile Gly Trp
 1090 1095 1100
 Lys Asp Tyr Thr Ala Tyr Arg Trp His Leu Thr His Arg Pro Lys Thr
 1105 1110 1115 1120
 Gly Tyr Ile Arg Val Leu Val His Glu Gly Lys Gln Val Met Ala Asp
 1125 1130 1135
 Ser Gly Pro Ile Tyr Asp Gln Thr Tyr Ala Gly Gly Arg Leu Gly Leu
 1140 1145 1150
 Phe Val Phe Ser Gln Glu Met Val Tyr Phe Ser Asp Leu Lys Tyr Glu
 1155 1160 1165
 Cys Arg Asp Ile
 1170

<210> 3
 <211> 17
 <212> DNA
 <213> Homo sapiens

<400> 3
 aatggaackc agagatg

6/6

<210> 4
<211> 17
<212> DNA
<213> Homo sapiens

<400> 4
aaatgtagyg actgtca

17